Align two sequences

Mon Mar 21 03:24:27 "GMT 2005

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 /usr/tmp/seq1.100209.sca :  432 aa
>/usr/tmp/seq1.100209  [Unknown form], 432 bases,   432 aa vs. 019957-015920; SEQ ID NO:4
>/usr/tmp/seq2.100209  [Unknown form], 446 bases,   446 aa       019957-019400; SEQ ID NO:16
scoring matrix: , gap penalties: -12/-2
80.2% identity;            Global alignment score: 2357

          10        20        30        40        50
/usr/t MFQPLLDAFIESAPLKKWPLNLPP-LKIAVANMWGDEEIKKPKKSVLYFILSQHYTITLH
       ::::::::..::: ..:   . :: :::::::::::::.:::::::::.::.::..::
/usr/t MFQPLLDAYVESASIEKMASKSPPPLKIAVANMWGDEEIKEFKKSVLYFIFSQRYTIALH
          10        20        30        40        50        60

      60        70        80        90       100       110
/usr/t RNPDKPADIVFGNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL
       .::.. ..::.:::::::::::::::::::::::::::::::::::::::::::::::::::
/usr/t QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGENEVPNFNLFDYAIGFDELDFRDRYL
          70        80        90       100       110       120

      120       130       140       150       160       170
/usr/t RMPLYYAYLHYKAELVNDTTSPYKLQPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKR
       :::::: ::.::: :::::::::::. .:::.:::::.:::::::::::::::::.:::::::
/usr/t RMPLYYDRLHHKAESVNDTTSPYKLKDNSLYTLKKPSHQFKENHPNLCAVVNDESDPLKR
          130       140       150       160       170       180

      180       190       200       210       220       230
/usr/t GFASFVASNPNAPRRNAFYEALNAIEPVAGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
       : .:::::: ::: :::::.:::.:::::.:::::::::::::::::::::::::::::::
/usr/t GVVSFVASNANAPMRNAFYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKFNLCFEN
          190       200       210       220       230       240

      240       250       260       270       280       290
/usr/t TQGYGYVTEKIIDAYFSHTIPIYWGSPSVAKDFNPKSFVNVHDFNMFDEAIDYIRYLHTH
       .:::::::.:::::::::::::::::::::::::::::: :::::::::::::::::.::::
/usr/t SQGYGYVTEKILDAYFSHTIPIYWGSPSVAKDFNPKEFVNVHDFNMFDEAIDYIKYLHTH
          250       260       270       280       290       300

      300       310       320.       330       340       350
/usr/t PNAYLDMHYENPLNTIDGKAYFYQNLSFKKILDFFKTILENDTIYHDNP--FIFYRDLNE
       :::::: ::::::..:::::::.::::::: :::::::::::::::: : ... ::.:
/usr/t PNAYLDMGLYENPLNALDGKAYFYQDLSFKKILAFFKTILENDTIYHKSSTSFMWECDLDE
          310       320       330       340       350       360

      360       370       380       390                     400
/usr/t PSVSIDGLRVNYDDLRVNYDDLRVNYDDLRVNY--------------ERLLQNASPLLEL
       : .::: :::::::::::::::::::::::::::::          :::::::::::::
/usr/t PLASIDGLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYERLLQNASPLLEL
          370       380       390       400       410       420

      410       420       430
/usr/t SQNTTFKIYRKAYQKSLPLLRAIRRWVKK
       :::.:::::::::: :.. .
/usr/t SQNTSFKIYRKAYQK--PI-KNPYPYCAP
          430       440

Elapsed time:  0:00:00
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Exhibit A